

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph on page 1, spanning lines 2-3, with the following amended paragraph:

POLYNUCLEOTIDES ENCODING COCCIDIAN PARASITE CASEIN KINASE I, AS-A
CHEMOTHERAPEUTIC TARGET FOR ANTIPROTOZOAL AGENTS.

Please replace the paragraph spanning pages 40-41 with the following amended paragraph:

A series of nested PCR primers was designed and used to amplify cDNA fragments from tachyzoite RNA by RT-PCR. RNA was prepared with an Oligo (dT)₂₅ Dynabeads® kit (Dyna; Lake Success, NY) and a first-strand cDNA pool synthesized with superscript II (Invitrogen; Carlsbad, CA). PCR products were cloned with a TA cloning kit (Promega; Madison, WI) and sequenced. Most of the PCR products obtained corresponded to the original EST sequence. However, one of the three sets of PCR primer pairs used, GATATCAAACAGATAACTTTCTTCTCGGC (SEQ ID NO:9) and CAAGGAGCGGCAGTAGTGCAAGT (SEQ ID NO:10), also amplified a second class of cDNA product which showed greater homology to the CKI- α isoform of *Plasmodium falciparum* (Barik, S. et al., 1997, *supra*). The two distinct cDNA fragments were used separately to probe a tachyzoite cDNA library (#1896, NIH AIDS Research and Reference Reagent Program). Putative open reading frames were assigned based on sequence alignments of previously characterized CKI enzymes (Klimczak, L.J. et al., 1995, *supra*; Barik et al, 1997, *supra*; Gross and Anderson, 1998, *supra*; Moreno-Bueno, G. et al., 2000, *supra*), and the presence of an optimal nucleotide context surrounding potential translational start sites was identified (Seeber, F., 1997, *Parasitol. Res.* 83:309-311). Corresponding full-length clones were obtained and designated " α " or " β " based on their relative homology to malaria isoform PfCKI α . At least four different full-length clones with 5' untranslated nucleotide sequences extending beyond the predicted start site were obtained for each isoform. No cDNAs corresponding to potentially functional splice variants were detected. Since corresponding TgCKI " α " or " β " genomic contigs identified in the *Toxoplasma* genome database do not overlap (<http://www.toxodb.org/ToxoDB.shtml>), the genes appear to map to separate loci.